



## SEQUENCE LISTING

## GENERAL INFORMATION:

- (i) APPLICANT: Robert G. Ulrich,  
Mark A. Olson  
Sina Bavari
- (ii) TITLE OF INVENTION: Bacterial Superantigen  
Vaccines
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Charles H. Harris  
(B) STREET: US Army MPMC -504 Scott Street  
MCMR-JA (Charles H. Harris-Patent  
Atty)  
(C) CITY: FORT DETRICK  
(D) STATE: MARYLAND  
(E) COUNTRY: USA  
(F) ZIP: 21702-5012
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Macintosh  
(C) OPERATING SYSTEM: Macintosh 7.5  
(D) SOFTWARE: Microsoft Word 6.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/882,431  
(B) FILING DATE: June 25, 1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Charles H. Harris  
(B) REGISTRATION NUMBER: 34,616  
(C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION  
(A) TELEPHONE: (301) 619-2065  
(B) TELEFAX: (301) 619-7714
- (2) INFORMATION FOR SEQUENCE ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 830  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAAAAAAA CAGCATTTAC ATTACTTTTA TTCATTGCCC	40
TAACGTTGAC AACAAAGTCCA CTTGTAAATG GTAGCGAGAA	80
AAGCGAAGAA ATAAATGAAA AAGATTTGCG AAAAAAGTCT	120
GAATTGCAGG GAACAGCTTT AGGCAATCTT AAACAAATCT	160
ATTATTACAA TGAAAAAGCT AAAACTGAAA ATAAAGAGAG	200
TCACGATCAA TTTCGACAGC ATACTATATT GTTTAAAGGC	240
TTTTTTTACAG ATCATTCGTG GTATAACGAT TTATTAGTAC	280
GTTTTGATTC AAAGGATATT GTTGATAAAT ATAAAGGGAA	320
AAAAGTAGAC TTGTATGGTG CTTATGCTGG TTATCAATGT	360
GCGGGTGGTA CACCAAACAA AACAGCTTGT ATGTATGGTG	400
GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA	440
AAAAGTGCCG ATCAATTTAT GGCTAGACGG TAAACAAAAT	480
ACAGTACCTT TGGAAACGGT TAAAACGAAT AAGAAAAATG	520
TAACTGTTCA GGAGTTGGAT CTTCAAGCAA GACGTTATTT	560
ACAGGAAAAA TATAATTTAT ATAACCTCTGA TGTTTTTGAT	600
GGGAAGGTTT AGAGGGGATT AATCGTGTTT CATACTTCTA	640
CAGAACCTTC GGTTAATTAC GATTTATTTG GTGCTCAAGG	680
ACAGTATTCA AATACACTAT TAAGAATATA TAGAGATAAT	720
AAAACGATTA ACTCTGAAAA CATGCATATT GATATATATT	760
TATATACAAG TTAAACATGG TAGTTTTGAC CAACGTAATG	800
TTCAGATTAT TATGAACCGA GAATAATCTA	830

(3) INFORMATION FOR SEQUENCE ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257

(B) TYPE: Amino Acid  
 (C) STRANDEDNESS: Unknown  
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Lys	Thr	Ala	Phe	Thr	Leu	Leu	Leu	1	5	10
Phe	Ile	Ala	Leu	Thr	Leu	Thr	Thr	Ser	Pro	15		20
Leu	Val	Asn	Gly	Ser	Glu	Lys	Ser	Glu	Glu	25		30
Ile	Asn	Glu	Lys	Asp	Leu	Arg	Lys	Lys	Ser	35		40
Glu	Leu	Gln	Gly	Thr	Ala	Leu	Gly	Asn	Leu	45		50
Lys	Gln	Ile	Tyr	Tyr	Tyr	Asn	Glu	Lys	Ala	55		60
Lys	Thr	Glu	Asn	Lys	Glu	Ser	His	Asp	Gln	65		70
Phe	Arg	Gln	His	Thr	Ile	Leu	Phe	Lys	Gly	75		80
Phe	Phe	Thr	Asp	His	Ser	Trp	Tyr	Asn	Asp	85		90
Leu	Leu	Val	Arg	Phe	Asp	Ser	Lys	Asp	Ile	95		100
Val	Asp	Lys	Tyr	Lys	Gly	Lys	Lys	Val	Asp	105		110
Leu	Tyr	Gly	Ala	Tyr	Ala	Gly	Tyr	Gln	Cys	115		120
Ala	Gly	Gly	Thr	Pro	Asn	Lys	Thr	Ala	Cys	125		130
Met	Tyr	Gly	Gly	Val	Thr	Leu	His	Asp	Asn	135		140
Asn	Arg	Leu	Thr	Glu	Glu	Lys	Lys	Val	Pro	145		150
Ile	Asn	Leu	Trp	Leu	Asp	Gly	Lys	Gln	Asn	155		160

Thr Val Pro Leu	Glu Thr Val Lys Thr Asn	
165		170
Lys Lys Asn Val	Thr Val Gln Glu Leu Asp	
175		180
Leu Gln Ala Arg	Arg Tyr Leu Gln Glu Lys	
185		190
Tyr Asn Leu Tyr	Asn Ser Asp Val Phe Asp	
195		200
Gly Lys Val Gln	Arg Gly Leu Ile Val Phe	
205		210
His Thr Ser Thr	Glu Pro Ser Val Asn Tyr	
215		220
Asp Leu Phe Gly	Ala Gln Gly Gln Tyr Ser	
225		230
Asn Thr Leu leu	Arg Ile Tyr Arg Asp Asn	
235		240
Lys Thr Ile Asn	Ser Glu Asn Met His Ile	
245		250
Asp Ile Tyr Leu	Tyr Thr Ser	
255		

(4) INFORMATION FOR SEQUENCE ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAGAAAAG CGAAGAAATA AATGAAAAG ATTTGCGAAA	40
AAAGTCTGAA TTGCAGGGAA CAGCTTTAGG CAATCTTAAA	80
CAAATCTATT ATTACAATGA AAAAGCTAAA ACTGAAAATA	120
AAGAGAGTCA CGATCAATTT CGACAGCATA CTATATTGTT	160
TAAAGGCTTT TTTACAGATC ATTCGTGGTA TAACGATTTA	200

TTAGTACGTT TTGATTCAAA GGATATTGTT GATAAATATA 240  
 AAGGGAAAAA AGTAGACTTG TATGGTGCTT ATGCTGGTTA 280  
 TCAATGTGCG GGTGGTACAC CAAACAAAAC AGCTTGTATG 320  
 TATGGTGGTG TAACGTTACA TGATAATAAT CGATTGACCG 360  
 AAGAGAAAAA AGTGCCGATC AATTTATGGC TAGACGGTAA 400  
 ACAAATACA GTACCTTTGG AAACGGTTAA AACGAATAAG 440  
 AAAAATGTAA CTGTTCAGGA GTTGGATCTT CAAGCAAGAC 480  
 GTTATTTACA GGAAAAATAT AATTTATATA ACTCTGATGT 520  
 TTTTGATGGG AAGGTTTCTA GGGGATTAAT CGTGTTTCAT 560  
 ACTTCTACAG AACCTTCGGT TAATTACGAT TTATTTGGTG 600  
 CTCAAGGACA GTATTCAAAT AACTATTAA GAATATATAG 640  
 AGATAATAAA ACGATTAAC CTGAAACAT GCATATTGAT 680  
 ATATATTTAT ATACAAGTTA AACATGCTAG TTTTGACCAA 720  
 CGTAATGTTC AGATTATTAT GAACCGAGAA TAATCTA 757

(5) INFORMATION FOR SEQUENCE ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:233
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Lys Ser Glu Glu Ile Asn Glu Lys  
5 10

Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly  
15 20

Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr  
25 30

Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn  
35 40

Lys Glu Ser His Asp Gln Phe Arg Gln His  
45 50

Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp  
 55 60  
 His Ser Trp Tyr Asn Asp Leu Leu Val Arg  
 65 70  
 Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr  
 75 80  
 Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala  
 85 90  
 Tyr Ala Gly Tyr Gln Cys Ala Gly Gly Thr  
 95 100  
 Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly  
 105 110  
 Val Thr Leu His Asp Asn Asn Arg Leu Thr  
 115 120  
 Glu Glu Lys Lys Val Pro Ile Asn Leu Trp  
 125 130  
 Leu Asp Gly Lys Gln Asn Thr Val Pro Leu  
 135 140  
 Glu Thr Val Lys Thr Asn Lys Lys Asn Val  
 145 150  
 Thr Val Gln Glu Leu Asp Leu Gln Ala Arg  
 155 160  
 Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr  
 165 170  
 Asn Ser Asp Val Phe Asp Gly Lys Val Gln  
 175 180  
 Arg Gly Leu Ile Val Phe His Thr Ser Thr  
 185 190  
 Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly  
 195 200  
 Ala Gln Gly Gln Tyr Ser Asn Thr Leu Leu  
 205 210  
 Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn  
 215 220

GAAGTAGGTA	GAAGAAATAAT	TATGAGAAAA	CACATATGTTG	40
TTAAAGATGT	TTTCGTATAT	AAGTTTAGGT	GATGTATAGT	80
TACTTAATTT	TAAAAGCATA	ACTTAATTAA	TATAAATAAC	120
ATGAGATTAT	TAAATATAAT	TAAGTTTCTT	TTAATGTTTT	160
TTTAATTGAA	TATTTAAGAT	TATAACATAT	ATTTAAAGTG	200
TATCTAGATA	CTTTTTTGGA	ATGTTGGATA	AAGGAGATAA	240
AAAATGTATA	AGAGATTATT	TATTTACAT	GTAATTTTGA	280
TATTCGCACT	GATATTAGTT	ATTTCTACAC	CCAACGTTTT	320
AGCAGAGAGT	CAACCAGATC	CTAAACCAGA	TGAGTTGCAC	360
AAATCGAGTA	AATTCACTGG	TTTGATGGAA	GATATGAAAG	400
TTTTGTATGA	TGATAATCAT	GTATCAGCAA	TAAACGTAA	440
ATCTATAGAT	CAATTTCTAT	ACTTTGACTT	AATATATTCT	480
ATTAAGGACA	CTAAGTTAGG	GGATTATGAT	AATGTTTCGAG	520
TCGAATTTAA	AAACAAAGAT	TTAGCTGATA	AATACAAAGA	560
TAAATACGTA	GATGTGTTTG	GAGCTAATTA	TTATTATCAA	600
TGTTATTTTT	CTAAAAAAC	GAATGATATT	AATTCGCATC	640
AAACTGACAA	ACGAAAAACT	TGTATGTATG	GTGGTGTAAC	680

TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT	720
ACTGTTCCGGG TATTTGAAGA TGGTAAAAAT TTATTATCTT	760
TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
ATTAGATTAC CTAACTCGTC ACTATTTGGT GAAAAATAAA	840
AAACTCTATG AATTTAACAA CTCGCCTTAT GAAACGGGAT	880
ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
CATGATGCCT GCACCAGGAG ATAAATTTGC CCAATCTAAA	960
TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
AATTAAGGCA GGCACCTATA GAGTACCTGC CTTTCTAAT	1120
ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
TAGCATTAAAC CCCTTGTTGC CATTATAGTT TTCACCAACT	1200
TTAGCTGAAA TTGGGGGATC ATTTTATCT TTAATATGGA	1240
TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTCTCTTTT	1280
TAATTTGTCA GTTAATTTTT TCCATGCATC ATTTGCGTCA	1320
AACCTATTTT CATTGATT TATTCTTGAC AAATCAATTC	1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAAAATT	1400
ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT	1480
CATTGCTGT TTTATCGATA ATATTGCTT CTTCAAAGC	1520
ATCTCTTACA TTTTCCATA AGTCTCTATC TGTATTTC	1560
GAAGCCTTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AACTAAAGC	1640
ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCATT	1680
TTATTTTCTC CTATAACTTA TTTGCAATCG AT	1712



## (7) INFORMATION FOR SEQUENCE ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

## (ii) Molecule type: Peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Tyr	Lys	Arg	Leu	Phe	Ile	Ser	His	Val		
				5					10		
Ile	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Val	Ile		
				15					20		
Ser	Thr	Pro	Asn	Val	Leu	Ala	Glu	Ser	Gln		
				25					30		
Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys		
				35					40		
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asp		
				45					50		
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val		
				55					60		
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln		
				65					70		
Phe	Leu	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile		
				75					80		
Lys	Asp	Thr	Lys	Leu	Gly	Asp	Tyr	Asp	Asn		
				85					90		
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu		
				95					100		
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp		
				105					110		
Val	Phe	Gly	Ala	Asn	Tyr	Tyr	Tyr	Gln	Cys		
				115					120		
Tyr	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn		
				125					130		
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys		
				135					140		

Met Tyr Gly Gly Val Thr Glu His Asn Gly	145	150
Asn Gln Leu Asp Lys Tyr Arg Ser Ile Thr	155	160
Val Arg Val Phe Glu Asp Gly Lys Asn Leu	165	170
Leu Ser Phe Asp Val Gln Thr Asn Lys Lys	175	180
Lys Val Thr Ala Gln Glu Leu Asp Tyr Leu	185	190
Thr Arg His Tyr Leu Val Lys Asn Lys Lys	195	200
Leu Tyr Glu Phe Asn Asn Ser Pro Tyr Glu	205	210
Thr Gly Tyr Ile Lys Phe Ile Glu Asn Glu	215	220
Asn Ser Phe Trp Tyr Asp Met Met Pro Ala	225	230
Pro Gly Asp Lys Phe Ala Gln Ser Lys Tyr	235	240
Leu Met Met Tyr Asn Asp Asn Lys Met Val	245	250
Asp Ser Lys Asp Val Lys Ile Glu Val Tyr	255	260
Leu Thr Thr Lys Lys Lys	265	

## (8) INFORMATION FOR SEQUENCE ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGTAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG

TTAAAGATGT	TTTCGTATAT	AAGTTTAGGT	GATGTATAGT	80
TACTTAATTT	TAAAAGCATA	ACTTAATTAA	TATAAATAAC	120
ATGAGATTAT	TAAATATAAT	TAAGTTTCTT	TTAATGTTTT	160
TTTAATTGAA	TATTTAAGAT	TATAACATAT	ATTTAAAGTG	200
TATCTAGATA	CTTTTTGGGA	ATGTTGGATA	AAGGAGATAA	240
AAAATGTATA	AGAGATTATT	TATTTACACAT	GTAATTTTGA	280
TATTCGCACT	GATATTAGTT	ATTTCTACAC	CCAACGTTTT	320
AGCAGAGAGT	CAACCAGATC	CTAAACCAGA	TGAGTTGCAC	360
AAATCGAGTA	AATTCACGG	TTTGATGGAA	AATATGAAAG	400
TTTTGTATGA	TGATAATCAT	GTATCAGCAA	TAAACGTTAA	440
ATCTATAGAT	CAATTTTCGAT	ACTTTGACTT	AATATATTCT	480
ATTAAGGACA	CTAAGTTAGG	GAATTATGAT	AATGTTTCGAG	520
TCGAATTTAA	AAACAAAGAT	TTAGCTGATA	AATACAAAGA	560
TAAATACGTA	GATGTGTTTG	GAGCTAATGC	TTATTATCAA	600
TGTGCTTTTT	CTAAAAAAC	GAATGATATT	AATTCGCATC	640
AAACTGACAA	ACGAAAAACT	TGTATGTATG	GTGGTGTAAC	680
TGAGCATAAT	GGAAACCAAT	TAGATAAATA	TAGAAGTATT	720
ACTGTTTCGGG	TATTTGAAGA	TGGTAAAAAT	TTATTATCTT	760
TTGACGTACA	AACTAATAAG	AAAAAGGTGA	CTGCTCAAGA	800
ATTAGATTAC	CTAACTCGTC	ACTATTTGGT	GAAAAATAAA	840
AAACTCTATG	AATTTAACAA	CTCGCCTTAT	GAAACGGGAT	880
ATATTAAATT	TATAGAAAAT	GAGAATAGCT	TTTGGTATGA	920
CATGATGCCT	GCACCAGGAG	ATAAATTTGA	CCAATCTAAA	960
TATTTAATGA	TGTACAATGA	CAATAAAATG	GTTGATTCTA	1000
AAGATGTGAA	GATTGAAGTT	TATCTTACGA	CAAAGAAAAA	1040
GTGAAATTAT	ATTTTAGAAA	AGTAAATATG	AAGAGTTAGT	1080
AATTAAGGCA	GGCACTTATA	GAGTACCTGC	CTTTTCTAAT	1120

ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT	1160
TAGCATTAAC CCCTTGTTGC CATTATAGTT TTCACCAACT	1200
TTAGCTGAAA TTGGGGGATC ATTTTTATCT TTACTATGGA	1240
TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTTCTCTTT	1280
TAATTTGTCA GTTAATTTTT TCCATGCATC ATTTGCGTCA	1320
AACCTATTTT CATTGGGATT TATTCTTGAC AAATCAATTC	1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAATAATT	1400
ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT	1440
TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT	1480
CATTTGCTGT TTTATCGATA ATATTGCTT CTTTCAAAGC	1520
ATCTCTTACA TTTTCCATA AGTCTCTATC TGTTATTTCA	1560
GAAGCCTTTG CAACGTTATT AATACCATTA TAATTTGAAG	1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AAATAAAGC	1640
ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCATT	1680
TTATTTTCTC CTATAACTTA TTTGCAATCG AT	1712

(9) INFORMATION FOR SEQUENCE ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Tyr Lys Arg Leu Phe Ile Ser His Val	
	5 10
Ile Leu Ile Phe Ala Leu Ile Leu Val Ile	
	15 20
Ser Thr Pro Asn Val Leu Ala Glu Ser Gln	
	25 30

Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys	35	40
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asn	45	50
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val	55	60
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln	65	70
Phe	Arg	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile	75	80
Lys	Asp	Thr	Lys	Leu	Gly	Asn	Tyr	Asp	Asn	85	90
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu	95	100
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp	105	110
Val	Phe	Gly	Ala	Asn	Ala	Tyr	Tyr	Gln	Cys	115	120
Ala	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn	125	130
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys	135	140
Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly	145	150
Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr	155	160
Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu	165	170
Leu	Ser	Phe	Asp	Val	Gln	Tyr	Asn	Lys	Lys	175	180
Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu	185	190
Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys	195	200
Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu	205	210

Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Glu		
				215					220		
Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala		
				225					230		
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr		
				235					240		
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val		
				245					250		
Asp	Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr		
				255					260		
Leu	Thr	Thr	Lys	Lys	Lys						
				265							

(10) INFORMATION FOR SEQUENCE ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGTCAAC CAGATCCTAA ACCAGATGAG TTGCACAAAT	40
CGAGTAAATT CACTGGTTTG ATGGAAAATA TGAAAGTTTT	80
GTATGATGAT AATCATGTAT CAGCAATAAA CGTTAAATCT	120
ATAGATCAAT TTCGATACTT TGACTTAATA TATTCTATTA	160
AGGACACTAA GTTAGGGAAT TATGATAATG TTCGAGTCGA	200
ATTTAAAAAC AAAGATTTAG CTGATAAATA CAAAGATAAA	240
TACGTAGATG TGTTTGGAGC TAATGCTTAT TATCAATGTG	280
CTTTTTCTAA AAAAACGAAT GATATTAATT CGCATCAAAC	320
TGACAAACGA AAAACTTGTA TGTATGGTGG TGTAAGTGG	360
CATAATGGAA ACCAATTAGA TAAATATAGA AGTATTACTG	400
TTCGGGTATT TGAAGATGGT AAAAATTAT TATCTTTTGA	440

CGTACAACT AATAAGAAAA AGGTGACTGC TCAAGAATTA	480
GATTACCTAA CTCGTCAC TA TTTGGTGAAA AATAAAAAAC	520
TCTATGAATT TAACAAC TCG CCTTATGAAA CGGGATATAT	560
TAAATTTATA GAAAATGAGA ATAGCTTTTG GTATGACATG	600
ATGCCTGCAC CAGGAGATAA ATTTGACCAA TCTAAATATT	640
TAATGATGTA CAATGACAAT AAAATGGTTG ATTCTAAAGA	680
TGTGAAGATT GAAGTTTATC TTACGACAAA GAAAAAGTGA	720
AATTATATTT TAGAAAAGTA AATATGAAGA GTTAGTAATT	760
AAGGCAGGCA CTTATAGAGT ACCTGCCTTT TCTAATATTA	800
TTTAGTTATA GTTATTTTTG TTATATCTCT CTGATTTAGC	840
ATTAACCCCT TGTGTCATT ATAGTTTTCAC CAACTTTAG	880
CTGAAATTGG GGGATCATT TTATCTTTAC TATGGATAGT	920
TACTGTGTCG CCGTTTTTAA CGATTGTTT CTCTTTTAAT	960
TTGTCAGTTA ATTTTTTCCA TGCATCATT GCGTCAAACC	1000
TATTTCCATT TGGATTATT CTTGACAAAT CAATTCTTTT	1040
AACACTATCG GTATTAATCG GCTTGTTATT AAAATTACTA	1080
AGTTCATCTA AATCAGCTGT ACCCGTAATA CTACTTTCGC	1120
CACCATTATT TAAATTGTAC GTAACACCAA CTGTCTCATT	1160
TGCTGTTTTA TCGATAATAT TTGCTTCTTT CAAAGCATCT	1200
CTTACATTTT TCCATAAGTC TCTATCTGTT ATTTGAGAAG	1240
CCTTTGCAAC GTTATTAATA CCATTATAAT TTGAAGAAGA	1280
ATGAAAACCT GAACCTACTG TTGTTAAAAC TAAAGCACTT	1320
GCTATCAATG TTCTTGTTAA TAGTTTTTTA TTCATTTTAT	1360
TTTCTCCTAT AACTTATTTG CAATCGAT	1388

(11) INFORMATION FOR SEQUENCE ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239

(B) TYPE: Amino Acid  
 (C) STRANDEDNESS: Unknown  
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Gln	Pro	Asp	Pro	Lys	Pro	Asp	Glu	5	10
Leu	His	Lys	Ser	Ser	Lys	Phe	Thr	Gly	Leu	15	20
Met	Glu	Asn	Met	Lys	Val	Leu	Tyr	Asp	Asp	25	30
Asn	His	Val	Ser	Ala	Ile	Asn	Val	Lys	Ser	35	40
Ile	Asp	Gln	Phe	Arg	Tyr	Phe	Asp	Leu	Ile	45	50
Tyr	Ser	Ile	Lys	Asp	Thr	Lys	Leu	Gly	Asn	55	60
Tyr	Asp	Asn	Val	Arg	Val	Glu	Phe	Lys	Asn	65	70
Lys	Asp	Leu	Ala	Asp	Lys	Tyr	Lys	Asp	Lys	75	80
Tyr	Val	Asp	Val	Phe	Gly	Ala	Asn	Ala	Tyr	85	90
Tyr	Gln	Cys	Ala	Phe	Ser	Lys	Lys	Thr	Asn	95	100
Asp	Ile	Asn	Ser	His	Gln	Thr	Asp	Lys	Arg	105	110
Lys	Thr	Cys	Met	Tyr	Gly	Gly	Val	Thr	Glu	115	120
His	Asn	Gly	Asn	Gln	Leu	Asp	Lys	Tyr	Arg	125	130
Ser	Ile	Thr	Val	Arg	Val	Phe	Glu	Asp	Gly	135	140
Lys	Asn	Leu	Leu	Ser	Phe	Asp	Val	Gln	Thr	145	150
Asn	Lys	Lys	Lys	Val	Thr	Ala	Gln	Glu	Leu		



	155		160
Asp Tyr Leu Thr Arg His Tyr Leu Val Lys			
	165		170
Asn Lys Lys Leu Tyr Glu Phe Asn Asn Ser			
	175		180
Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile			
	185		190
Glu Asn Glu Asn Ser Phe Trp Tyr Asp Met			
	195		200
Met Pro Ala Pro Gly Asp Lys Phe Asp Gln			
	205		210
Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn			
	215		220
Lys Met Val Asp Ser Lys Asp Val Lys Ile			
	225		230
Glu Val Tyr Leu Thr Thr Lys Lys Lys			
	235		

(12) INFORMATION FOR SEQUENCE ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAAGGAGAAT TAAAAATGAA TAAAAAATTA CTAATGAATT	40
TTTTTATCGT AAGCCCTTTG TTGCTTGCGA CAACTGCTAC	80
AGATTTTACC CCTGTTCCCT TATCATCTAA TCAAATAATC	120
AAAAGTGCAA AAGCATCTAC AAACGATAAT ATAAAGGATT	160
TGCTAGACTG GTATAGTAGT GGGTCTGACA CTTTACAAA	200
TAGTGAAGTT TTAGATAATT CCAGAGGATC TATGCGTATA	240
AAAAACACAG ATGGCAGCAT CAGCTTGATA ATTTTCCGA	280

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GTCCTTATTA TAGCCCTGCT TTTACAAAAG GGGAAAAAGT    320
TGACTTAAAC ACAAAAAGAA CTAAAAAAG CCAACATACT    360
AGCGAAGGAA CTTATATCCA TTTCCAAATA AGTGGCGTTA    400
CAAATACTGA AAAATTACCT ACTCCAATAG AACTACCTTT    440
AAAAGTTAAG GTTCATGGTA AAGATAGCCC CTAAAGTAT    480
GGGCCAAAGT TCGATAAAAA ACAATTAGCT ATATCAACTT    520
TAGACTTTGA AATTCGTCAT CAGCTAACTC AAATACATGG    560
ATTATATCGT TCAAGCGATA AAACGGGTGG TTATTGGAAA    600
ATAACAATGA ATGACGGATC CACATATCAA AGTGATTTAT    640
CTAAAAAGTT TGAATACAAT ACTGAAAAAC CACCTATAAA    680
TATTGATGAA ATAAAAACTA TAGAAGCAGA AATTAATTAA    720
TTTACCACTT T                                     731

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(13) INFORMATION FOR SEQUENCE ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Asn Lys Lys Leu Leu Met Asn Phe Phe
      5                               10

Ile Val Ser Pro Leu Leu Leu Ala Thr Thr
      15                           20

Ala Thr Asp Phe Thr Pro Val Pro Leu Ser
      25                           30

Ser Asn Gln Ile Ile Lys Thr Ala Lys Ala
      35                           40

Ser Thr Asn Asp Asn Ile Lys Asp Leu Leu
      45                           50

Asp Trp Tyr Ser Ser Gly Ser Asp Thr Phe
      55                           60

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Thr	Asn	Ser	Glu	Val	Leu	Asp	Asn	Ser	Arg	
				65					70	
Gly	Ser	Met	Arg	Ile	Lys	Asn	Thr	Asp	Gly	
				75					80	
Ser	Ile	Ser	Leu	Ile	Ile	Phe	Pro	Ser	Pro	
				85					90	
Tyr	Tyr	Ser	Pro	Ala	Phe	Thr	Lys	Gly	Glu	
				95					100	
Lys	Val	Asp	Leu	Asn	Thr	Lys	Arg	Thr	Lys	
				105					110	
Lys	Ser	Gln	His	Thr	Ser	Glu	Gly	Thr	Tyr	
				115					120	
Ile	His	Phe	Gln	Ile	Ser	Gly	Val	Thr	Asn	
				125					130	
Thr	Glu	Lys	Leu	Pro	Thr	Pro	Ile	Glu	Leu	
				135					140	
Pro	Leu	Lys	Val	Lys	Val	His	Gly	Lys	Asp	
				145					150	
Ser	Pro	Leu	Lys	Tyr	Gly	Pro	Lys	Phe	Asp	
				155					160	
Lys	Lys	Gln	Leu	Ala	Ile	Ser	Thr	Leu	Asp	
				165					170	
Phe	Glu	Ile	Arg	His	Gln	Leu	Thr	Gln	Ile	
				175					180	
His	Gly	Leu	Tyr	Arg	Ser	Ser	Asp	Lys	Thr	
				185					190	
Gly	Gly	Tyr	Trp	Lys	Ile	Thr	Met	Asn	Asp	
				195					200	
Gly	Ser	Thr	Tyr	Gln	Ser	Asp	Leu	Ser	Lys	
				205					210	
Lys	Phe	Glu	Tyr	Asn	Thr	Glu	Lys	Pro	Pro	
				215					220	
Ile	Asn	Ile	Asp	Glu	Ile	Lys	Thr	Ile	Glu	
				225					230	
Ala	Glu	Ile	Asn							

## (14) INFORMATION FOR SEQUENCE ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

## (ii) Molecule type: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCATTAAAT ATAATTAATT TTCTTTTAAT ATTTTTTTAA	40
TTGAATATTT AAGATTATAA GATATATTTA AAGTGATCT	80
AGATACTTTT TGGGAATGTT GGATGAAGGA GATAAAAATG	120
AATAAGAGTC GATTTATTTT ATGCGTAATT TTGATATTCG	160
CACTTATACT AGTTCTTTTT ACACCCAACG TATTAGCAGA	200
GAGCCAACCA GACCCTACGC CAGATGAGTT GCACAAAGCG	240
AGTAAATTCA CTGGTTTGAT GGAAAATATG AAAGTTTTAT	280
ATGATGATCA TTATGTATCA GCAACTAAAG TTAAGTCTGT	320
AGATAAATTT AGGGCACATG ATTTAATTTA TAACATTAGT	360
GATAAAAAAC TGAAAAATTA TGACAAAGTG AAAACAGAGT	400
TATTAAATGA AGGTTTAGCA AAGAAGTACA AAGATGAAGT	440
AGTTGATGTG TATGGATCAA ATTACTATGT AACTGCTAT	480
TTTTCATCCA AAGATAATGT AGGTAAAGTT ACAGGTGGCA	520
AAACTTGTAT GTATGGAGGA ATAACAAAAC ATGAAGGAAA	560
CCACTTTGAT AATGGGAACT TACAAAATGT ACTTATAAGA	600
GTTTATGAAA ATAAAAGAAA CACAATTTCT TTTGAAGTGC	640
AAACTGATAA GAAAAGTGTA ACAGCTCAAG AACTAGACAT	680
AAAAGCTAGG AATTTTTTTAA TTAATAAAAA AAATTTGTAT	720
GAGTTTAAAC GTTCACCATA TGAAACAGGA TATATAAAAT	760
TTATTGAAAA TAACGGCAAT ACTTTTGGT ATGATATGAT	800

GCCTGCACCA GCGGATAAGT TTGACCAATC TAAATATTTA	840
ATGATGTACA ACGACAATAA AACGGTTGAT TCTAAAAGTG	880
TGAAGATAGA AGTCCACCTT ACAACAAAGA ATGGATAATG	920
TTAATCCGAT TTTGATATAA AAAGTGAAAG TATTAGATAT	960
ATTTGAAAGG TAAGTACTTC GGTGCTTGCC TTTTtaggAT	1000
GCATATATAT AGATTAAACC GCACTTCTAT ATTAATAGAA	1040
AGTGCGGTTA TTTATACACT CAATCTAAAC TATAATAATT	1080
GGAATCATCT TCAAA	1095

## (15) INFORMATION FOR SEQUENCE ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asn Lys Ser Arg Phe Ile Ser Cys Val	
	5 10
Ile Leu Ile Phe Ala Leu Ile Leu Val Leu	
	15 20
Phe Thr Pro Asn Val Leu Ala Glu Ser Gln	
	25 30
Pro Asp Pro Thr Pro Asp Glu Leu His Lys	
	35 40
Ala Ser Lys Phe Thr Gly Leu Met Glu Asn	
	45 50
Met Lys Val Leu Tyr Asp Asp His Tyr Val	
	55 60
Ser Ala Thr Lys Val Lys Ser Val Asp Lys	
	65 70
Phe Arg Ala His Asp Leu Ile Tyr Asn Ile	
	75 80

Ser	Asp	Lys	Lys	Leu	Lys	Asn	Tyr	Asp	Lys	85	90
Val	Lys	Thr	Glu	Leu	Leu	Asn	Glu	Gly	Leu	95	100
Ala	Lys	Lys	Tyr	Lys	Asp	Glu	Val	Val	Asp	105	110
Val	Tyr	Gly	Ser	Asn	Tyr	Tyr	Val	Asn	Cys	115	120
Tyr	Phe	Ser	Ser	Lys	Asp	Asn	Val	Gly	Lys	125	130
Val	Thr	Gly	Gly	Lys	Thr	Cys	Met	Tyr	Gly	135	140
Gly	Ile	Thr	Lys	His	Glu	Gly	Asn	His	Phe	145	150
Asp	Asn	Gly	Asn	Leu	Gln	Asn	Val	Leu	Ile	155	160
Arg	Val	Tyr	Glu	Asn	Lys	Arg	Asn	Thr	Ile	165	170
Ser	Phe	Glu	Val	Gln	Thr	Asp	Lys	Lys	Ser	175	180
Val	Thr	Ala	Gln	Glu	Leu	Asp	Ile	Lys	Ala	185	190
Arg	Asn	Phe	Leu	Ile	Asn	Lys	Lys	Asn	Leu	195	200
Tyr	Glu	Phe	Asn	Ser	Ser	Phe	Tyr	Glu	Thr	205	210
Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Asn	Gly	215	220
Asn	Thr	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala	225	230
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr	235	240
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Thr	Val	245	250
Asp	Ser	Lys	Ser	Val	Lys	Ile	Glu	Val	His	255	260

Leu Thr Thr Lys Asn Gly  
265

(16) INFORMATION FOR SEQUENCE ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCATGTTTGA CAGCTTATCA TCGATAAGCT TACTTTTCGA	40
ATCAGGTCTA TCCTTGAAAC AGGTGCAACA TAGATTAGGG	80
CATGGAGATT TACCAGACAA CTATGAACGT ATATACTCAC	120
ATCACGCAAT CGGCAATTGA TGACATTGGA ACTAAATTCA	160
ATCAATTTGT TACTAACAAG CAACTAGATT GACAACTAAT	200
TCTCAACAAA CGTTAATTTA ACAACATTCA AGTAACTCCC	240
ACCAGCTCCA TCAATGCTTA CCGTAAGTAA TCATAACTTA	280
CTAAACCTT GTTACATCAA GGTTTTTTCT TTTTGTCTTG	320
TTCATGAGTT ACCATAACTT TCTATATTAT TGACAACATA	360
ATTGACAACT CTTCAATTAT TTTTCTGTCT ACTCAAAGTT	400
TTCTTCATTT GATATAGTCT AATTCCACCA TCACTTCTTC	440
CACTCTCTCT ACCGTCACAA CTTTCATCAT TCTCACTTTT	480
TCGTGTGGTA ACACATAATC AAATATCTTT CCGTTTTTAC	520
GCACTATCGC TACTGTGTCA CCTAAAATAT ACCCCTTATC	560
AATCGCTTCT TTAAACTCAT CTATATATAA CATATTCAT	600
CCTCCTACCT ATCTATTCGT AAAAAGATAA AAATAACTAT	640
TGTTTTTTTT GTTATTTTAT AATAAAATTA TTAATATAAG	680
TTAATGTTTT TTAAAAATAT ACAATTTTAT TCTATTTATA	720

GTTAGCTATT	TTTTCATTGT	TAGTAATATT	GGTGAATTGT	760
AATAACCTTT	TTAAATCTAG	AGGAGAACCC	AGATATAAAA	800
TGGAGGAATA	TTAATGGAAA	ACAATAAAAA	AGTATTGAAG	840
AAAATGGTAT	TTTTTGTTTT	AGTGACATTT	CTTGGACTION	880
CAATCTCGCA	AGAGGTATTT	GCTCAACAAG	ACCCCGATCC	920
AAGCCAACTT	CACAGATCTA	GTTTAGTTAA	AAACCTTCAA	960
AATATATATT	TTCTTTATGA	GGGTGACCCT	GTTACTCACG	1000
AGAATGTGAA	ATCTGTTGAT	CAACTTAGAT	CTCACGATTT	1040
AATATATAAT	GTTTCAGGGC	CAAATTATGA	TAAATTAAAA	1080
ACTGAACTTA	AGAACCAAGA	GATGGCAACT	TTATTTAAGG	1120
ATAAAAACGT	TGATATTTAT	GGTGTAGAAT	ATTACCATCT	1160
CTGTTATTTA	TGTGAAAATG	CAGAAAGGAG	TGCATGTATC	1200
TACGGAGGGG	TAACAAATCA	TGAAGGGAAT	CATTTAGAAA	1240
TTCTTAAAAA	GATAGTCGTT	AAAGTATCAA	TCGATGGTAT	1280
CCAAAGCCTA	TCATTTGATA	TTGAAACAAA	TAAAAAAATG	1320
GTAACGCTC	AAGAATTAGA	CTATAAAGTT	AGAAAATATC	1360
TTACAGATAA	TAAGCAACTA	TATACTAATG	GACCTTCTAA	1400
ATATGAAACT	GGATATATAA	AGTTCATACC	TAAGAATAAA	1440
GAAAGTTTTT	GGTTTGATTT	TTTCCCTGAA	CCAGAATTTA	1480
CTCAATCTAA	ATATCTTATG	ATATATAAAG	ATAATGAAAC	1520
GCTTGACTCA	AACACAAGCC	AAATTGAAGT	CTACCTAACA	1560
ACCAAGTAAC	TTTTTGCTTT	TGGCAACCTT	ACCTACTGCT	1600
GGATTTAGAA	ATTTTATTGC	AATTCTTTTA	TTAATGTAAA	1640
AACCGCTCAT	TTGATGAGCG	GTTTTGTCTT	ATCTAAAGGA	1680
GCTTTACCTC	CTAATGCTGC	AAAATTTTAA	ATGTTGGATT	1720
TTTGTATTTG	TCTATTGTAT	TTGATGGGTA	ATCCCATTTT	1760
TCGACAGACA	TCGTCGTGCC	ACCTCTAACA	CCAAAATCAT	1800



AGACAGGAGC TTGTAGCTTA GCAACTATTT TATCGTC

1837

## (17) INFORMATION FOR SEQUENCE ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Glu	Asn	Asn	Lys	Lys	Val	Leu	Lys	Lys	5	10
Met	Val	Phe	Phe	Val	Leu	Val	Thr	Phe	Leu	15	20
Gly	Leu	Thr	Ile	Ser	Gln	Glu	Val	Phe	Ala	25	30
Gln	Gln	Asp	Pro	Asp	Pro	Ser	Gln	Leu	His	35	40
Arg	Ser	Ser	Leu	Val	Lys	Asn	Leu	Gln	Asn	45	50
Ile	Tyr	Phe	Leu	Tyr	Glu	Gly	Asp	Pro	Val	55	60
Thr	His	Glu	Asn	Val	Lys	Ser	Val	Asp	Gln	65	70
Leu	Arg	Ser	His	Asp	Leu	Ile	Tyr	Asn	Val	75	80
Ser	Gly	Pro	Asn	Tyr	Asp	Lys	Leu	Lys	Thr	85	90
Glu	Leu	Lys	Asn	Gln	Glu	Met	Ala	Thr	Leu	95	100
Phe	Lys	Asp	Lys	Asn	Val	Asp	Ile	Tyr	Gly	105	110
Val	Glu	Tyr	Tyr	His	Leu	Cys	Tyr	Leu	Cys	115	120
Glu	Asn	Ala	Glu	Arg	Ser	Ala	Cys	Ile	Tyr	125	130
Gly	Gly	Val	Thr	Asn	His	Glu	Gly	Asn	His		

135 140  
 Leu Glu Ile Pro Lys Lys Ile Val Val Lys  
 145 150  
 Val Ser Ile Asp Gly Ile Gln Ser Leu Ser  
 155 160  
 Phe Asp Ile Glu Thr Asn Lys Lys Met Val  
 165 170  
 Thr Ala Gln Glu Leu Asp Tyr Lys Val Arg  
 175 180  
 Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr  
 185 190  
 Thr Asn Gly Pro Ser Lys Tyr Glu Thr Gly  
 195 200  
 Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu  
 205 210  
 Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro  
 215 220  
 Glu Phe Thr Gln Ser Lys Tyr Leu Met Ile  
 225 230  
 Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn  
 235 240  
 Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr  
 245 250  
 Lys

B6  
 cont